

RAW SEQUENCE LISTING **ERROR REPORT**

8
BIOTECHNOLOGY
- SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/151,409
Art Unit / Team No. : 1645
Date Processed by STIC: 1/29/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/15/409

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.
- 7 Wrong Designation Sequence(s) contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (1) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of N's or Xaa's Use of N's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) 16 are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
 (Sec. 1.823 of new Sequence Rules)
- 13 Wrong Format File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the
 "Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures"
 Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620
 applies to applications filed on or after July 1, 1998.
 AKS-Biotechnology Systems Branch- 7/10/98

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RAW SEQUENCE LISTING
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This Raw Listing contains the General Information
Section and up to first 5 pages.

see
p.5
Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Dale, James B.
2 <120> TITLE OF INVENTION: GROUP A STREPTOCOCCAL VACCINES
3 <130> FILE REFERENCE: 481112.410
4 <140> CURRENT APPLICATION NUMBER: US/09/151,409
5 <141> CURRENT FILING DATE: 1998-09-10
6 <150> EARLIER APPLICATION NUMBER: US 60/058,635
7 <151> EARLIER FILING DATE: 1997-09-12
8 <160> NUMBER OF SEQ ID NOS: 16
9 <170> SOFTWARE: PatentIn Ver. 2.0
10 <210> SEQ ID NO 1
11 <211> LENGTH: 36
12 <212> TYPE: DNA
13 <213> ORGANISM: Artificial Sequence
14 <220> FEATURE:
15 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
16 Synthesis -- Primer, hybridizes to streptococcal
17 type 24 M protein DNA
18 <400> SEQUENCE: 1 36
19 gggggggcat cggtcgcgac taggtctcag acagat
20 <210> SEQ ID NO 2
21 <211> LENGTH: 30
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
26 Synthesis -- Primer, hybridizes to streptococcal
27 type 24 M protein DNA
28 <400> SEQUENCE: 2 30
29 ggggggggat ccacgtagtt tctctttagc
30 <210> SEQ ID NO 3
31 <211> LENGTH: 30
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
35 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
36 Synthesis -- Primer, hybridizes to streptococcal
37 type 5 M protein DNA
38 <400> SEQUENCE: 3 30
39 ggggggggat ccgccgtgac taggggtaca
40 <210> SEQ ID NO 4
41 <211> LENGTH: 30
42 <212> TYPE: DNA
43 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:

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45 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
46 Synthesis -- Primer, hybridizes to streptococcal
47 type 5 M protein DNA
48 <400> SEQUENCE: 4 30
49 gggggggtcg acctcagttt ttaacccttc
50 <210> SEQ ID NO 5
51 <211> LENGTH: 30
52 <212> TYPE: DNA
53 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
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57 type 6 M protein DNA
58 <400> SEQUENCE: 5 30
59 gggggggtcg acagagtgtt tcctaggggg
60 <210> SEQ ID NO 6
61 <211> LENGTH: 30
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
64 <220> FEATURE:
65 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
66 Synthesis -- Primer, hybridizes to streptococcal
67 type 6 M protein DNA
68 <400> SEQUENCE: 6 30
69 gggggggccat ggtaacttgt cattattagc
70 <210> SEQ ID NO 7
71 <211> LENGTH: 30
72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
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75 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
76 Synthesis -- Primer, hybridizes to streptococcal
77 type 19 M protein DNA
78 <400> SEQUENCE: 7 30
79 gggggggccat ggagagtgcg ttatactagg
80 <210> SEQ ID NO 8
81 <211> LENGTH: 30
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
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87 type 19 M protein DNA
88 <400> SEQUENCE: 8 30
89 gggggggctgc agagataact tctcattctg
90 <210> SEQ ID NO 9
91 <211> LENGTH: 30
92 <212> TYPE: DNA
93 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:

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95 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
96 Synthesis -- Primer, hybridizes to streptococcal
97 type 1 M protein DNA
98 <400> SEQUENCE: 9 30
99 ggggggctgc agaacggtga tggtaatcct
100 <210> SEQ ID NO 10
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103 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
106 Synthesis -- Primer, hybridizes to streptococcal
107 type 1 M protein DNA
108 <400> SEQUENCE: 10 30
109 ggggggggta ccagctctct taaaatctct
110 <210> SEQ ID NO 11
111 <211> LENGTH: 30
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
116 Synthesis -- Primer, hybridizes to streptococcal
117 type 3 M protein DNA
118 <400> SEQUENCE: 11 30
119 ggggggggta ccttggttaga tcagggtaca
120 <210> SEQ ID NO 12
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122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
124 <220> FEATURE:
125 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
126 Synthesis -- Primer, hybridizes to streptococcal
127 type 3 M protein DNA
128 <400> SEQUENCE: 12 30
129 ggggggatcg atatttaact cttgtaacag
130 <210> SEQ ID NO 13
131 <211> LENGTH: 30
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
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137 type 24 M protein DNA
138 <400> SEQUENCE: 13 30
139 ggggggatcg atgtcgcgac taggtctcag
140 <210> SEQ ID NO 14
141 <211> LENGTH: 33
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:

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145 <223> OTHER INFORMATION: Description of Artificial Sequence: Product of
146 Synthesis -- Primer, hybridizes to streptococcal
147 type 24 M protein DNA
148 <400> SEQUENCE: 14
149 ggggggaagc ttttacttac gtgcctctaa ttc 33
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151 <211> LENGTH: 1158
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Description of Artificial Sequence: Hexavalent M
156 fusion gene sequence constructed from
157 streptococcal type 24, 5, 6, 19, 1 and 3 M protein
158 DNAs
159 <220> FEATURE:
160 <221> NAME/KEY: CDS
161 <222> LOCATION: (1)..(1149)
162 <400> SEQUENCE: 15
163 gca tgc atg gtc gcg act agg tct cag aca gat act ctg gaa aaa gta 48
164 Ala Cys Met Val Ala Thr Arg Ser Gln Thr Asp Thr Leu Glu Lys Val
165 1 5 10 15
166 caa gaa cgt gct gac aag ttt gag ata gaa aac aat acg tta aaa ctt 96
167 Gln Glu Arg Ala Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu
168 20 25 30
169 aag aat agt gac tta agt ttt aat aat aaa gcg tta aaa gat cat aat 144
170 Lys Asn Ser Asp Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn
171 35 40 45
172 gat gag tta act gaa gag ttg agt aat gct aaa gag aaa cta cgt gga 192
173 Asp Glu Leu Thr Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Gly
174 50 55 60
175 tcc gcc gtg act agg ggt aca ata aat gac ccg caa aga gca aaa gaa 240
176 Ser Ala Val Thr Arg Gly Thr Ile Asn Asp Pro Gln Arg Ala Lys Glu
177 65 70 75 80
178 gct ctt gac aag tat gag cta gaa aac cat gac tta aaa act aag aat 288
179 Ala Leu Asp Lys Tyr Glu Leu Glu Asn His Asp Leu Lys Thr Lys Asn
180 85 90 95
181 gaa ggg tta aaa act gag aat gaa ggg tta aaa act gag aat gaa ggg 336
182 Glu Gly Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Asn Glu Gly
183 100 105 110
184 tta aaa act gag aat gaa ggg tta aaa act gag gtc gac aga gtg ttt 384
185 Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Val Asp Arg Val Phe
186 115 120 125
187 cct agg ggg acg gta gaa aac ccg gac aaa gca cga gaa ctt ctt aac 432
188 Pro Arg Gly Thr Val Glu Asn Pro Asp Lys Ala Arg Glu Leu Leu Asn
189 130 135 140
190 aag tat gac gta gag aac tct atg tta caa gct aat aat gac aag tta 480
191 Lys Tyr Asp Val Glu Asn Ser Met Leu Gln Ala Asn Asn Asp Lys Leu
192 145 150 155 160
193 cca tgg aga gtg cgt tat act agg cat acg cca gaa gat aag cta aaa 528
194 Pro Trp Arg Val Arg Tyr Thr Arg His Thr Pro Glu Asp Lys Leu Lys

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195          165          170          175
196  aaa att att gac gat ctt gac gca aaa gaa cat gaa tta caa caa cag 576
197  Lys Ile Ile Asp Asp Leu Asp Ala Lys Glu His Glu Leu Gln Gln Gln
198          180          185          190
199  aat gag aag tta tct ctg cag aac ggt gat ggt aat cct agg gaa gtt 624
200  Asn Glu Lys Leu Ser Leu Gln Asn Gly Asp Gly Asn Pro Arg Glu Val
201          195          200          205
202  ata gaa gat ctt gca gca aac aat ccc gca ata caa aat ata cgt tta 672
203  Ile Glu Asp Leu Ala Ala Asn Asn Pro Ala Ile Gln Asn Ile Arg Leu
204          210          215          220
205  cgt cac gaa aac aag gac tta aaa gcg aga tta gag aat gca atg gaa 720
206  Arg His Glu Asn Lys Asp Leu Lys Ala Arg Leu Glu Asn Ala Met Glu
207  225          230          235          240
208  gtt gca gga aga gat ttt aag aga gct ggt acc ttg tta gat cag gtt 768
209  Val Ala Gly Arg Asp Phe Lys Arg Ala Gly Thr Leu Leu Asp Gln Val
210          245          250          255
211  aca caa tta tat act aaa cat aat agt aat tac caa caa tat aat gca 816
212  Thr Gln Leu Tyr Thr Lys His Asn Ser Asn Tyr Gln Gln Tyr Asn Ala
213          260          265          270
214  caa gct ggc aga ctt gac ctg aga caa aag gct gaa tat cta aaa ggc 864
215  Gln Ala Gly Arg Leu Asp Leu Arg Gln Lys Ala Glu Tyr Leu Lys Gly
216          275          280          285
217  ctt aat gat tgg gct gag agg ctg tta caa gag tta aat atc gat gtc 912
218  Leu Asn Asp Trp Ala Glu Arg Leu Leu Gln Glu Leu Asn Ile Asp Val
219          290          295          300
220  gcg act agg tct cag aca gat act ctg gaa aaa gta caa gaa cgt gct 960
221  Ala Thr Arg Ser Gln Thr Asp Thr Leu Glu Lys Val Gln Glu Arg Ala
222  305          310          315          320
223  gac aag ttt gag ata gaa aac aat acg tta aaa ctt aag aat agt gac 1008
224  Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu Lys Asn Ser Asp
225          325          330          335
226  tta agt ttt aat aat aaa gcg tta aaa gat cat aat gat gag tta act 1056
227  Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn Asp Glu Leu Thr
228          340          345          350
229  gaa gag ttg agt aat gct aaa gag aaa cta cgt aaa aat gat aaa tca 1104
230  Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Lys Asn Asp Lys Ser
231          355          360          365
232  cta tct gaa aaa gct agt aaa att caa gaa tta gag gca cgt aag 1149
233  Leu Ser Glu Lys Ala Ser Lys Ile Gln Glu Leu Glu Ala Arg Lys
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235  taaaagctt 1158
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237  <211> LENGTH: 383
238  <212> TYPE: PRT
239  <213> ORGANISM: Artificial Sequence
240  <400> SEQUENCE: 16
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242  1 5 10 15
243  Gln Glu Arg Ala Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu
244  20 25 30

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see item 12 in Eva Summary sheet

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
